

ESTIMATION OF GENETIC VARIABILITY AND BREEDING VALUES, THE EFFECT OF SUBSTITUTION OF ALLELES AND THE AVERAGE EFFECT OF CAST GENE IN SOME CHARACTERISTICS OF GOAT CARCASSES

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ABSTRACT : The study was conducted on 93 Local goat males to determine the breeding values and the additive and dominant effects and Average effect of *CAST* gene substitution in the variation of the slaughter (SLW) and hot (HOT) weights of the carcasses and the rib eye area (REA) using the SNP information by the RFLP and the *MspI* Restriction enzymes. The breeding values (BV) of the MM genotype were higher than those of the MN for SLW and REA of the carcass which were 0.766 and 0.186 respectively, while it was higher for MN genotype(5.962) in HOT trait .Thus strengthening the selection trend on the basis of MM genotype to raise the average weight of carcasses . Also, the dominant variation within the genetic variance was higher than the additive variance, reaching 10.598 and 0.599 for SLW and REA traits respectively indicating the strength of the initial reaction and its effect on the average characteristics. The average of the allele effect and the effect of substitution of alleles were all in favor of the M alleles compare to mutant allele (N), which encourages the selection against the mutant allele.

Key words : Breeding value, genetic variance, alleles substitute, calpastatin gene.

INTRODUCTION

The Calpastatin gene (*CAST*) affects muscle growth and its post-slaughter pattern significantly and it is a gene located on the goat's fifth chromosome (1), a major inhibitor of calpain enzyme post-slaughter activity that regulates the ratio and extent of meat tenderness after slaughter (2). Genetic improvement using selection by genetic markers and genome information is primarily based on the additive effect, which plays an important role in influencing the physiology and evolution of farm animals (3). As that, the dominant effect has added value to the additive variation in the studied character variation, so many studies have begun to shed Highlight this effect (of the dominant variation) role in the total variation of complex productivity traits (4, 5, 6). In order to understand the genetic content and genetic characteristics of the population/herd, a genetic analysis of the variation components, particularly the additive (VA), which represents the breeding value and dominance deviation (VD) and Interaction Deviation (VI) must be done (7). Although the study of genetic maps has largely focused on additive genetic variation, many studies have stressed the importance of non-negligible contribution of non-

additive effects in QTL (8). The different aspects of the different genotypes are mainly due to the pure or hybrid image of the alleles, in another meaning, the amount of the contribution of each allele negatively or positively in the phenotype of the character and the genetic selection in general, but the redistribution of the proportions of these alleles among individuals in order to increase replication at the level of the individual or herd,therefor, its consider an attempt to replace the unwanted allele with another one in the same locus has the most effect, known as the effect of substitution of alleles (7). Live weight is a measure and approximation of the weight in which animals are slaughtered to reach a certain fat level by which animal or carcass value can be predicted for commercial purposes, also the weight of the carcass is an indicator and a key criterion for determining the market class of meat and determining differences in carcass components and components of carcass cuts (9). The researchers pointed out that live weight, hot and cold carcass weights reflect the weights and percentages of different tissues in the carcass, muscle size, weights and percentages of carcass cuts (10, 11). Estimate of rib eye area is an indicator of the amount of muscling in carcass because it is directly

correlated with the amount of muscles in the carcass (12), genetic evaluation of goats, bucks and their kids based on growth rate is part of many goat development and body weight is an important indicate for breeding programs (13,14).

The aim of this research is to estimate the breeding values, calculate the total genetic variance and determine the additive and dominant variability as well as the effect of the effect of substitution of alleles and the average effect of cast gene in slaughter and hot weights and REA characteristics in Local goat carcasses.

MATERIALS AND METHODS

The study included 93 male local goats aged 10 months in order to collect blood samples, slaughter them and measure carcass traits. The blood sample (3 ml) was extracted from the jugular vein from each animal in test tubes containing K2EDTA coagulation inhibitor and placed in a container Refrigerated tubes and transferred to the laboratory for freezing at -18°C until the time of extraction of DNA from them. The process of slaughter (according to the Islamic method in Iraq) included all the animals involved in the experiment (93 goats) after starving them for 12 hours by cutting the fodder and leaving the water available to them.

Slaughter live weight

Slaughter live weight (SLW) was measured immediately before slaughter, where the animal is weighed and then slaughtered immediately.

Hot carcass weight

The weight of the hot carcass (HOT) was calculated after about one hour of the slaughter process using a suspended weighing scale of 50 kg .

Rib eye area

The Rib eye area (REA) was drawn in the area

between the twelfth and thirteenth ribs on the left side of carcass using semi-transparent wax paper. The REA is calculated using the planimeter and the average of two readings of the cross section are taken.

Amplifications of DNA fragments and PCR-RFLP

Two primer pairs [5'-CCT TGT CAT CAGACT TCA CC-3' (forward) and 5'-ACT GAG CTT TTAAAG CCT CT-3' (reverse)] were employed targeting a fragment of 565bp as described by (15) to find out the M and N alleles of *CAST* gene.

The PCR reactions were performed on an ABI Veritithermo cycler and the PCR cycling condition was a preliminary denaturing at 95°C for 5 min., then, followed by 1 cycle of denaturing at 94°C for 0.5 min., annealing at 55°C for 0.5 min., and extension at 72°C for 0.5 min. by 35 cycles and finally followed by 7 min. at 72°C as a extension. The amplified fragment of *CAST* gene was digested by the restriction endonuclease *MspI* (BROMIGA CO.). The next step was the separated of digested products by electrophoresis on 2% (v/w) agarose gel stained with Safe View (NBS Biological, UK) Electrophoresis was performed in a 1X TBE buffer at room temperature and constant 70 V for 90 min.

Statistical analysis

The equations for each calculated value were applied as follows (7):

1. The average effect of allele A = $q[a+d(q-p)] = \alpha A$
2. The average effect of allele B = $-p[a+d(q-p)] = \alpha B$
3. The effect of substitution of alleles = $\alpha A - \alpha B$
4. The breeding values : $AA=2\alpha 1, AB=\alpha 1+\alpha 2, BB=2\alpha 2$
5. The dominant deviations : $AA=2q^2 d, AB=2pqd, BB=2p^2 d$

Table 1 : Breeding value, dominance deviation and genetic variations of genotypes in *CAST* gene for slaughter live weight (SLW), rib eye area (REA) and hot carcass weight (HOT) traits.

SLW						
Genotype	Mean	BV	DD	VA	VD	VG
MM	23.924	0.766	0.551	1.702	10.598	12.300
MN	25.102	-1.875	-3.258			
REA						
MM	5.868	0.186	0.131	0.102	0.599	0.701
MN	6.056	-0.457	-0.774			
HOT						
MM	9.542	2.494	-0.227	18.385	1.798	20.183
MN	10.18	5.962	-1.341			

BV: Breeding value, DD: dominance deviation , VA: Additive variance, VD: Dominance variance, VG: Genetic variance.

Table 2 : The average gene effect and the Average effect of gene substitution of alleles for slaughter live weight(SLW),rib eye area(REA) and hot carcass weight(HOT) traits

Trait	Alleles	Average gene effect	Average effect of gene substitution
SLW	M	0.383	2.642
	N	-2.258	-2.642
REA	M	0.930	0.644
	N	-0.550	-0.644
HOT	M	1.248	8.611
	N	-7.462	-8.611

6. The different variances : $VA=2pq \alpha^2$, $VD=4p^2q^2d^2$, $VG=VA+VD$

RESULTS

After RFLP- PCR conducting, two genotypes of the studied *CAST* gene fragment in Local Iraqi Goats were found to be the MM and MN, with $P = 0.855$ and $q = 0.145$, respectively. The MM was superior in terms of the breeding value of the next generation of SLM and REA traits, while the hybrid genotype of MN was superior in the hot weight of carcass trait (table 1). The dominant deviations (DD) were less than the breeding values of the MM genotype for all the studied traits. The additive variance (VA) "as a part of total genetic variance" was less than the dominant variance (VD) in SLW and REA traits, which reflecting the level of allelic interaction between alleles in *CAST* gene and its high contribution to total genetic variation. In the case of the hot carcass weight characteristic, the VA value (18.38) was higher than VD value (1.79) (Table 1). The average effect of M allele was positive for all studied traits, In contrast to mutant allele (N) which was negative (Table 2). The average effect of gene substitution for the studied traits was positive for M allele and negative for N allele (Table 2).

DISCUSSION

Results show that MM genotype can be selected to improve both slaughter live weight and rib eye area traits in goats because breeding values are the true value inherited by offspring, which can be used to select parents to the next generation (18). The reliance on the selection which based on estimated breeding values using genetic markers increases the annual genetic yield by reducing generation interval, increasing accuracy and reducing cost (19). The interaction between the allelic genes is evident in the studied traits by increasing the VD value at the expense of the VA value within the total genetic variation. However, this does not eliminate the additive effect but explains the high value of the hybrid genotype (3, 18) and the value of VA remains the true one of the gene that

will inherit and remain influential despite the existence of the dominance and epistasis effects (7). The value of the average allele and the average substitution of allele M was positive and high, confirming its importance as a genetic marker in the selection programs for the studied traits, as this value represents the value added as a result of the election, which is affected by the frequency of the allele (7, 19, 20).

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